# Phyre$^2$

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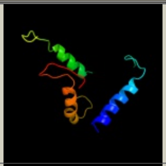
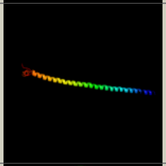
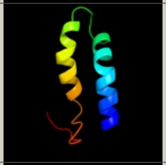
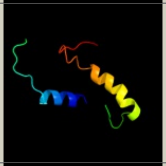
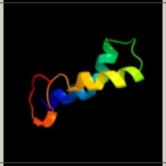
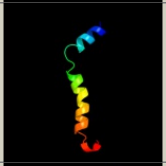
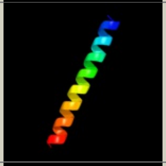
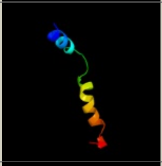
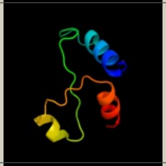
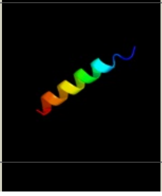
| Email | l.a.kelley@imperial.ac.uk |
| Description | Q46793 |
| Date | Thu Jan 5 12:34:14 GMT 2012 |
| Unique Job ID | d5701b779f521790 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2g62A_ | Alignment |  | 83.5 | 21 | **PDB header:**hydrolase activator<br>**Chain:** A: **PDB Molecule:**protein phosphatase 2a, regulatory subunit b' (pr 53);<br>**PDBTitle:** crystal structure of human ptpa |
| 2 | c3k5bE_ | Alignment |  | 80.4 | 14 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**v-type atp synthase subunit e;<br>**PDBTitle:** crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase |
| 3 | d2ixoa1 | Alignment |  | 67.7 | 14 | **Fold:**PTPA-like<br>**Superfamily:**PTPA-like<br>**Family:**PTPA-like |
| 4 | d2ixma1 | Alignment |  | 66.2 | 21 | **Fold:**PTPA-like<br>**Superfamily:**PTPA-like<br>**Family:**PTPA-like |
| 5 | d2ixna1 | Alignment |  | 50.8 | 14 | **Fold:**PTPA-like<br>**Superfamily:**PTPA-like<br>**Family:**PTPA-like |
| 6 | c2yhbA_ | Alignment |  | 37.0 | 20 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**post-transcriptional gene silencing protein qde-2;<br>**PDBTitle:** crystal structure of the n. crassa qde-2 ago mid-piwi domains |
| 7 | c2k88A_ | Alignment |  | 34.1 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**vacuolar proton pump subunit g;<br>**PDBTitle:** association of subunit d (vma6p) and e (vma4p) with g2 (vma10p) and the nmr solution structure of subunit g (g1-3 59) of the saccharomyces cerevisiae v1vo atpase |
| 8 | c2yhaA_ | Alignment |  | 33.7 | 20 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**post-transcriptional gene silencing protein qde-2;<br>**PDBTitle:** crystal structure of the n. crassa qde-2 ago mid-piwi2 domains |
| 9 | d1wmha_ | Alignment |  | 32.9 | 19 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**CAD & PB1 domains<br>**Family:**PB1 domain |
| 10 | c2ktrA_ | Alignment |  | 24.6 | 14 | **PDB header:**signaling protein, transport protein<br>**Chain:** A: **PDB Molecule:**sequestosome-1;<br>**PDBTitle:** nmr structure of p62 pb1 dimer determined based on pcs |
| 11 | c1p0oA_ | Alignment |  | 22.3 | 21 | **PDB header:**ribosome<br>**Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1;<br>**PDBTitle:** hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles |

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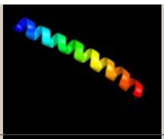
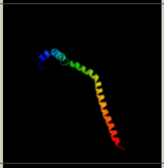
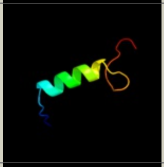
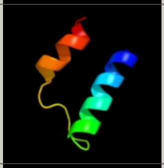
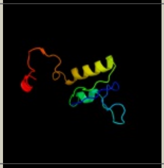
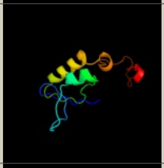
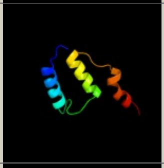
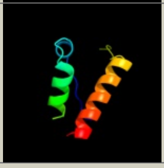
| 12 | c2kk7A_ | Alignment |  | 21.9 | 9 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**v-type atp synthase subunit e;<br>**PDBTitle:** nmr solution structure of the n terminal domain of subunit e2 (e1-52) of a1ao atp synthase from methanocaldococcus3 jannaschii |
| 13 | c4a1aC_ | Alignment |  | 20.3 | 11 | **PDB header:**ribosome<br>**Chain:** C: **PDB Molecule:**rpl4;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3. |
| 14 | c3smaD_ | Alignment |  | 19.8 | 19 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**frbf;<br>**PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf |
| 15 | d2csba1 | Alignment |  | 19.0 | 47 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**Topoisomerase V repeat domain |
| 16 | c2r18A_ | Alignment |  | 19.0 | 25 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**capsid assembly protein vp3;<br>**PDBTitle:** structural insights into the multifunctional protein vp3 of2 birnaviruses |
| 17 | d2zkmx4 | Alignment |  | 18.5 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLC-like phosphodiesterases<br>**Family:**Mammalian PLC |
| 18 | d1qasa3 | Alignment |  | 18.2 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**PLC-like phosphodiesterases<br>**Family:**Mammalian PLC |
| 19 | c3ebqA_ | Alignment |  | 17.2 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**molecule: pppde1 (permuted papain fold<br>**PDBTitle:** crystal structure of human pppde1 |
| 20 | d1mo0a_ | Alignment |  | 16.0 | 33 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Triosephosphate isomerase (TIM)<br>**Family:**Triosephosphate isomerase (TIM) |
| 21 | d1mr1c_ | Alignment | not modelled | 15.5 | 23 | **Fold:**SAND domain-like<br>**Superfamily:**SAND domain-like<br>**Family:**SMAD4-binding domain of oncoprotein Ski |
| 22 | c3c18B_ | Alignment | not modelled | 15.1 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**nucleotidyltransferase-like protein;<br>**PDBTitle:** crystal structure of nucleotidyltransferase-like protein2 (zp_00538802.1) from exiguobacterium sibiricum 255-15 at 1.90 a3 resolution |
| 23 | c3kbgA_ | Alignment | not modelled | 14.5 | 18 | **PDB header:**ribosomal protein<br>**Chain:** A: **PDB Molecule:**30s ribosomal protein s4e;<br>**PDBTitle:** crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28. |
| 24 | d2od6a1 | Alignment | not modelled | 14.4 | 33 | **Fold:**Ferredoxin-like<br>**Superfamily:**Dimeric alpha+beta barrel<br>**Family:**Marine metagenome family DABB1 |
| 25 | c2jrmA_ | Alignment | not modelled | 14.3 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**ribosome modulation factor;<br>**PDBTitle:** solution nmr structure of ribosome modulation factor vp1593 from2 vibrio parahaemolyticus. northeast structural genomics target vpr55 |
| 26 | d2uz9a1 | Alignment | not modelled | 14.0 | 29 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**SAH/MTA deaminase-like |
| 27 | c1djyB_ | Alignment | not modelled | 13.2 | 32 | **PDB header:**lipid degradation<br>**Chain:** B: **PDB Molecule:**phosphoinositide-specific phospholipase c,<br>**PDBTitle:** phosphoinositide-specific phospholipase c-delta1 from rat2 complexed with inositol-2,4,5-trisphosphate |
| 28 | d1ubea2 | Alignment | not modelled | 13.0 | 32 | **Fold:**Anti-LPS factor/recA domain<br>**Superfamily:**RecA protein, C-terminal domain |

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| | | | | | | **Family:**RecA protein, C-terminal domain |
| 29 | d1mo6a2 | Alignment | not modelled | 12.8 | 28 | **Fold:**Anti-LPS factor/recA domain<br>**Superfamily:**RecA protein, C-terminal domain<br>**Family:**RecA protein, C-terminal domain |
| 30 | c2qsjB_ | Alignment | not modelled | 12.8 | 13 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**dna-binding response regulator, luxr family;<br>**PDBTitle:** crystal structure of a luxr family dna-binding response2 regulator from silicibacter pomeroyi |
| 31 | c2q1kA_ | Alignment | not modelled | 12.7 | 27 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**asce;<br>**PDBTitle:** cyrstal structure of asce from aeromonas hydrophilla |
| 32 | d1ii2a2 | Alignment | not modelled | 12.6 | 19 | **Fold:**PEP carboxykinase N-terminal domain<br>**Superfamily:**PEP carboxykinase N-terminal domain<br>**Family:**PEP carboxykinase N-terminal domain |
| 33 | d1u94a2 | Alignment | not modelled | 12.5 | 32 | **Fold:**Anti-LPS factor/recA domain<br>**Superfamily:**RecA protein, C-terminal domain<br>**Family:**RecA protein, C-terminal domain |
| 34 | d1h3oa_ | Alignment | not modelled | 11.9 | 41 | **Fold:**Histone-fold<br>**Superfamily:**Histone-fold<br>**Family:**TBP-associated factors, TAFs |
| 35 | c1h3oA_ | Alignment | not modelled | 11.9 | 41 | **PDB header:**transcription/tbp-associated factors<br>**Chain:** A: **PDB Molecule:**transcription initiation factor tfiid 135 kda<br>**PDBTitle:** crystal structure of the human taf4-taf122 (tafii135-tafii20) complex |
| 36 | c2yy8B_ | Alignment | not modelled | 11.8 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**upf0106 protein ph0461;<br>**PDBTitle:** crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine |
| 37 | c3se4B_ | Alignment | not modelled | 11.7 | 11 | **PDB header:**immune system receptor<br>**Chain:** B: **PDB Molecule:**interferon omega-1;<br>**PDBTitle:** human ifnw-ifnar ternary complex |
| 38 | c3a2nF_ | Alignment | not modelled | 11.6 | 8 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**haloalkane dehalogenase;<br>**PDBTitle:** crystal structure of dbja (wild type type ii p21) |
| 39 | c2y6vB_ | Alignment | not modelled | 11.5 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**peroxisomal membrane protein lpx1;<br>**PDBTitle:** peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i) |
| 40 | c1m2zE_ | Alignment | not modelled | 11.3 | 37 | **PDB header:**hormone/hormone activator<br>**Chain:** E: **PDB Molecule:**nuclear receptor coactivator 2;<br>**PDBTitle:** crystal structure of a dimer complex of the human2 glucocorticoid receptor ligand-binding domain bound to3 dexamethasone and a tif2 coactivator motif |
| 41 | c3izcW_ | Alignment | not modelled | 11.3 | 17 | **PDB header:**ribosome<br>**Chain:** W: **PDB Molecule:**60s ribosomal protein rpl22 (l22e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 42 | c2fjuB_ | Alignment | not modelled | 11.3 | 28 | **PDB header:**signaling protein,apoptosis/hydrolase<br>**Chain:** B: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate<br>**PDBTitle:** activated rac1 bound to its effector phospholipase c beta 2 |
| 43 | c2xzmW_ | Alignment | not modelled | 11.0 | 24 | **PDB header:**ribosome<br>**Chain:** W: **PDB Molecule:**40s ribosomal protein s4;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |
| 44 | d1jyaa_ | Alignment | not modelled | 11.0 | 25 | **Fold:**Secretion chaperone-like<br>**Superfamily:**Type III secretory system chaperone-like<br>**Family:**Type III secretory system chaperone |
| 45 | c1m2zB_ | Alignment | not modelled | 10.8 | 37 | **PDB header:**hormone/hormone activator<br>**Chain:** B: **PDB Molecule:**nuclear receptor coactivator 2;<br>**PDBTitle:** crystal structure of a dimer complex of the human2 glucocorticoid receptor ligand-binding domain bound to3 dexamethasone and a tif2 coactivator motif |
| 46 | d1eg3a2 | Alignment | not modelled | 10.7 | 15 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**EF-hand modules in multidomain proteins |
| 47 | d1b5la_ | Alignment | not modelled | 10.3 | 13 | **Fold:**4-helical cytokines<br>**Superfamily:**4-helical cytokines<br>**Family:**Interferons/interleukin-10 (IL-10) |
| 48 | d1l2pa_ | Alignment | not modelled | 10.3 | 14 | **Fold:**Single transmembrane helix<br>**Superfamily:**F1F0 ATP synthase subunit B, membrane domain<br>**Family:**F1F0 ATP synthase subunit B, membrane domain |
| 49 | c2pd0D_ | Alignment | not modelled | 10.2 | 29 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** protein cgd2_2020 from cryptosporidium parvum |
| 50 | d1rh2a_ | Alignment | not modelled | 10.2 | 16 | **Fold:**4-helical cytokines<br>**Superfamily:**4-helical cytokines<br>**Family:**Interferons/interleukin-10 (IL-10) |
| 51 | c2dl1A_ | Alignment | not modelled | 10.0 | 10 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**spartin;<br>**PDBTitle:** solution structure of the mit domain from human spartin |
| 52 | c2dp3A_ | Alignment | not modelled | 9.8 | 22 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**triosephosphate isomerase;<br>**PDBTitle:** crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia |
| 53 | c3izbD_ | Alignment | not modelled | 9.5 | 20 | **PDB header:**ribosome<br>**Chain:** D: **PDB Molecule:**40s ribosomal protein rps4 (s4e);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into |

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| | | | | | | a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 54 | c1yyaA_ | Alignment | not modelled | 9.5 | 14 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**triosephosphate isomerase;<br>**PDBTitle:** crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8 |
| 55 | d1jrma_ | Alignment | not modelled | 9.3 | 21 | **Fold:**YggU-like<br>**Superfamily:**YggU-like<br>**Family:**YggU-like |
| 56 | d2jdia1 | Alignment | not modelled | 9.2 | 17 | **Fold:**Left-handed superhelix<br>**Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase<br>**Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase |
| 57 | c3iz6D_ | Alignment | not modelled | 9.2 | 6 | **PDB header:**ribosome<br>**Chain:** D: **PDB Molecule:**40s ribosomal protein s4 (s4e);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 58 | c3oaaO_ | Alignment | not modelled | 9.0 | 6 | **PDB header:**hydrolase/transport protein<br>**Chain:** O: **PDB Molecule:**atp synthase gamma chain;<br>**PDBTitle:** structure of the e.coli f1-atp synthase inhibited by subunit epsilon |
| 59 | c1r2fB_ | Alignment | not modelled | 9.0 | 12 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**protein (ribonucleotide reductase r2);<br>**PDBTitle:** ribonucleotide reductase r2f protein from salmonella2 typhimurium |
| 60 | c3ikmD_ | Alignment | not modelled | 8.9 | 26 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1;<br>**PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme |
| 61 | d1mj5a_ | Alignment | not modelled | 8.9 | 14 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloalkane dehalogenase |
| 62 | d1r2fa_ | Alignment | not modelled | 8.8 | 12 | **Fold:**Ferritin-like<br>**Superfamily:**Ferritin-like<br>**Family:**Ribonucleotide reductase-like |
| 63 | c2h0dB_ | Alignment | not modelled | 8.6 | 28 | **PDB header:**metal binding protein/ligase<br>**Chain:** B: **PDB Molecule:**ubiquitin ligase protein ring2;<br>**PDBTitle:** structure of a bmi-1-ring1b polycomb group ubiquitin ligase complex |
| 64 | d1asha_ | Alignment | not modelled | 8.6 | 14 | **Fold:**Globin-like<br>**Superfamily:**Globin-like<br>**Family:**Globins |
| 65 | d1q59a_ | Alignment | not modelled | 8.6 | 17 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Bcl-2 inhibitors of programmed cell death<br>**Family:**Bcl-2 inhibitors of programmed cell death |
| 66 | c3d8kD_ | Alignment | not modelled | 8.4 | 17 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**protein phosphatase 2c;<br>**PDBTitle:** crsytal structure of a phosphatase from a toxoplasma gondii |
| 67 | c4hb1A_ | Alignment | not modelled | 8.3 | 13 | **PDB header:**designed helical bundle<br>**Chain:** A: **PDB Molecule:**dhp1;<br>**PDBTitle:** a designed four helix bundle protein. |
| 68 | c2q8fA_ | Alignment | not modelled | 8.2 | 7 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 1;<br>**PDBTitle:** structure of pyruvate dehydrogenase kinase isoform 1 |
| 69 | d1nw3a_ | Alignment | not modelled | 8.1 | 14 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Catalytic, N-terminal domain of histone methyltransferase Dot1l |
| 70 | c1nw3A_ | Alignment | not modelled | 8.1 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**histone methyltransferase dot1l;<br>**PDBTitle:** structure of the catalytic domain of human dot1l, a non-set2 domain nucleosomal histone methyltransferase |
| 71 | d1xp8a2 | Alignment | not modelled | 7.8 | 16 | **Fold:**Anti-LPS factor/recA domain<br>**Superfamily:**RecA protein, C-terminal domain<br>**Family:**RecA protein, C-terminal domain |
| 72 | d1a77a1 | Alignment | not modelled | 7.8 | 15 | **Fold:**SAM domain-like<br>**Superfamily:**5' to 3' exonuclease, C-terminal subdomain<br>**Family:**5' to 3' exonuclease, C-terminal subdomain |
| 73 | c2yysA_ | Alignment | not modelled | 7.8 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**proline iminopeptidase-related protein;<br>**PDBTitle:** crystal structure of the proline iminopeptidase-related protein2 ttha1809 from thermus thermophilus hb8 |
| 74 | d1joga_ | Alignment | not modelled | 7.7 | 5 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Nucleotidyltransferase substrate binding subunit/domain<br>**Family:**Family 1 bi-partite nucleotidyltransferase subunit |
| 75 | c3eb7B_ | Alignment | not modelled | 7.7 | 10 | **PDB header:**toxin<br>**Chain:** B: **PDB Molecule:**insecticidal delta-endotoxin cry8ea1;<br>**PDBTitle:** crystal structure of insecticidal delta-endotoxin cry8ea1 from2 bacillus thuringiensis at 2.2 angstroms resolution |
| 76 | d1hx8a1 | Alignment | not modelled | 7.6 | 9 | **Fold:**Spectrin repeat-like<br>**Superfamily:**GAT-like domain<br>**Family:**Phosphoinositide-binding clathrin adaptor, domain 2 |
| 77 | d2jq9a1 | Alignment | not modelled | 7.6 | 13 | **Fold:**Spectrin repeat-like<br>**Superfamily:**MIT domain<br>**Family:**MIT domain |
| 78 | d1mzga_ | Alignment | not modelled | 7.6 | 21 | **Fold:**SufE/NifU<br>**Superfamily:**SufE/NifU<br>**Family:**SufE-like |
| 79 | d1k0wa_ | Alignment | not modelled | 7.6 | 17 | **Fold:**AraD/HMP-PK domain-like<br>**Superfamily:**AraD/HMP-PK domain-like |

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|---|---|---|---|---|---|---|
|  |  |  |  |  |  | **Family:**AraD-like aldolase/epimerase |
| 80 | c2xmzA_ | Alignment | not modelled | 7.5 | 14 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**hydrolase, alpha/beta hydrolase fold family;<br>**PDBTitle:** structure of menh from s. aureus |
| 81 | d1ttja_ | Alignment | not modelled | 7.5 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Triosephosphate isomerase (TIM)<br>**Family:**Triosephosphate isomerase (TIM) |
| 82 | c4a1dM_ | Alignment | not modelled | 7.5 | 20 | **PDB header:**ribosome<br>**Chain:** M: **PDB Molecule:**ribosomal protein l22;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4. |
| 83 | c3f6cB_ | Alignment | not modelled | 7.4 | 9 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**positive transcription regulator evga;<br>**PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli |
| 84 | c2rreA_ | Alignment | not modelled | 7.3 | 29 | **PDB header:**nuclear protein<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** structure and function of the n-terminal nucleolin binding domain of2 nuclear valocine containing protein like 2 (nvl2) harboring a3 nucleolar localization signal |
| 85 | c3e6qL_ | Alignment | not modelled | 7.3 | 20 | **PDB header:**isomerase<br>**Chain:** L: **PDB Molecule:**putative 5-carboxymethyl-2-hydroxymuconate isomerase;<br>**PDBTitle:** putative 5-carboxymethyl-2-hydroxymuconate isomerase from pseudomonas2 aeruginosa. |
| 86 | d1ea0a3 | Alignment | not modelled | 7.2 | 11 | **Fold:**Ntn hydrolase-like<br>**Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases)<br>**Family:**Class II glutamine amidotransferases |
| 87 | d1wfda_ | Alignment | not modelled | 7.1 | 16 | **Fold:**Spectrin repeat-like<br>**Superfamily:**MIT domain<br>**Family:**MIT domain |
| 88 | c3lruA_ | Alignment | not modelled | 7.0 | 18 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**pre-mrna-processing-splicing factor 8;<br>**PDBTitle:** hprp8 non-native subdomain |
| 89 | c2xoaA_ | Alignment | not modelled | 7.0 | 11 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**ryanodine receptor 1;<br>**PDBTitle:** crystal structure of the n-terminal three domains of the2 skeletal muscle ryanodine receptor (ryr1) |
| 90 | d1k3ia1 | Alignment | not modelled | 6.9 | 15 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**E set domains<br>**Family:**E-set domains of sugar-utilizing enzymes |
| 91 | d1fkma1 | Alignment | not modelled | 6.9 | 22 | **Fold:**Left-handed superhelix<br>**Superfamily:**Ypt/Rab-GAP domain of gyp1p<br>**Family:**Ypt/Rab-GAP domain of gyp1p |
| 92 | d2cw9a1 | Alignment | not modelled | 6.9 | 31 | **Fold:**Cystatin-like<br>**Superfamily:**NTF2-like<br>**Family:**TIM44-like |
| 93 | d1ukfa_ | Alignment | not modelled | 6.9 | 18 | **Fold:**Cysteine proteinases<br>**Superfamily:**Cysteine proteinases<br>**Family:**Avirulence protein Avrpph3 |
| 94 | d1ijdb_ | Alignment | not modelled | 6.9 | 17 | **Fold:**Light-harvesting complex subunits<br>**Superfamily:**Light-harvesting complex subunits<br>**Family:**Light-harvesting complex subunits |
| 95 | d1tuaa1 | Alignment | not modelled | 6.9 | 13 | **Fold:**Eukaryotic type KH-domain (KH-domain type I)<br>**Superfamily:**Eukaryotic type KH-domain (KH-domain type I)<br>**Family:**Eukaryotic type KH-domain (KH-domain type I) |
| 96 | c2o8gJ_ | Alignment | not modelled | 6.8 | 15 | **PDB header:**hydrolase/inhibitor<br>**Chain:** J: **PDB Molecule:**protein phosphatase inhibitor 2;<br>**PDBTitle:** rat pp1c gamma complexed with mouse inhibitor-2 |
| 97 | d2gpia1 | Alignment | not modelled | 6.7 | 14 | **Fold:**Shew3726-like<br>**Superfamily:**Shew3726-like<br>**Family:**Shew3726-like |
| 98 | c2z7bA_ | Alignment | not modelled | 6.6 | 6 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**mlr6791 protein;<br>**PDBTitle:** crystal structure of mesorhizobium loti 3-hydroxy-2-methylpyridine-4,2 5-dicarboxylate decarboxylase |
| 99 | c2rmrA_ | Alignment | not modelled | 6.5 | 21 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**paired amphipathic helix protein sin3a;<br>**PDBTitle:** solution structure of msin3a pah1 domain |